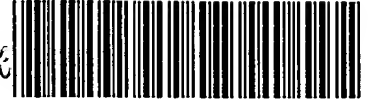


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RAW SEQUENCE LISTING

DATE: 09/15/2003

PATENT APPLICATION: US/09/194,164

TIME: 15:42:28

Input Set : N:\Crf3\RULE60\09194164.RAW.txt

Output Set: N:\CRF4\09152003\I194164.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Dan, Michael D.

6 Maiti, Pradip K.

7 Kaplan, Howard A.

9 (ii) TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT

10 SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING

THE 11 FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

12 DETECTION OF CANCERS

14 (iii) NUMBER OF SEQUENCES: 18

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Morrison & Foerster

18 (B) STREET: 755 Page Mill Road

19 (C) CITY: Palo Alto

20 (D) STATE: CA

21 (E) COUNTRY: USA

22 (F) ZIP: 94304-1018

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/194,164

C--> 32 (B) FILING DATE: 09-Apr-1999

33 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/657,449

38 (B) FILING DATE:

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Lehnhardt, Susan K.

43 (B) REGISTRATION NUMBER: 33,943

44 (C) REFERENCE/DOCKET NUMBER: 31608-20001.00

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (415) 813-5600

48 (B) TELEFAX: (415) 494-0792

49 (C) TELEX: 706141

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 543 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: double

58 (D) TOPOLOGY: linear

ENTERED

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Input Set : N:\Crif3\RULE60\09194164.RAW.txt

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62 (ix) FEATURE:

63 (A) NAME/KEY: CDS

64 (B) LOCATION: 1..543

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69	CAAGCTATTT	AGGTGACACT	ATAGAATACT	CAAGCTATGC	ATCCAACGCG	TTGGGAGCTC	60
71	TCCCATATGG	TCGACCTGCA	GGCGGCCGCA	CTAGTGATTT	CAAGCTTCAT	CACTGAACAC	120
73	AGAGGACTCA	CCATGGAGTT	TGGGCTGAGC	TGGGTTTTCC	TCGTTGCTCT	TTTAAGAGGT	180
75	ATCCAGTGTC	AGGTGCAGCT	GGTGGAGTCT	GGGGGAGGCG	TGGTCCAGCC	TGGGAGGTCC	240
77	CTGAGACTCT	CCTGTGCAGC	CTCTGGATTG	CCCTTCAGAA	GCTTTGCTAT	GCACTGGGTC	300
79	CGCCAGGCTC	TAGGCAAGGG	GCTGGAGTGG	GTGGCAGTTA	TATCATATGA	TGGAAGCACT	360
81	AAATACTACG	CAGACTCCGT	GAAGGGGCGA	TTCACCATCT	CCAGAGACAC	TTCCAAGAAC	420
83	ACGGTGTATC	TAAAAATGAA	CAGGCTGAGA	ACTGAGGACA	CGGCTGTCTT	TTACTTGTGC	480
85	GAAAGACAGA	GCCTGCTGGG	TGACTATGAC	CACTACTACG	GNTTGGACGC	TTGGGGAAAG	540
87	GGA						543

89 (2) INFORMATION FOR SEQ ID NO: 2:

91 (i) SEQUENCE CHARACTERISTICS:

92 (A) LENGTH: 179 amino acids

93 (B) TYPE: amino acid

94 (C) STRANDEDNESS: single

95 (D) TOPOLOGY: linear

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

103	Gln	Ala	Ile	Val	Thr	Leu	Asn	Thr	Gln	Ala	Met	His	Pro	Thr	Arg	Trp
104	1			5					10						15	
106	Glu	Leu	Ser	His	Met	Val	Asp	Leu	Gln	Ala	Ala	Ala	Leu	Val	Ile	Ser
107				20					25					30		
109	Ser	Phe	Ile	Thr	Glu	His	Arg	Gly	Leu	Thr	Met	Glu	Phe	Gly	Leu	Ser
110				35				40					45			
112	Trp	Val	Phe	Leu	Val	Ala	Leu	Leu	Arg	Gly	Ile	Gln	Cys	Gln	Val	Gln
113				50				55				60				
115	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg
116				65				70				75			80	
118	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Pro	Phe	Arg	Ser	Phe	Ala	Met	His
119					85					90					95	
121	Trp	Val	Arg	Gln	Ala	Leu	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile
122				100				105						110		
124	Ser	Tyr	Asp	Gly	Ser	Thr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg
125			115					120					125			
127	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Val	Tyr	Leu	Lys	Met
128			130					135					140			
130	Asn	Arg	Leu	Arg	Thr	Glu	Asp	Thr	Ala	Val	Phe	Tyr	Leu	Cys	Glu	Arg
131			145					150				155			160	
133	Gln	Ser	Leu	Leu	Gly	Asp	Tyr	Asp	His	Tyr	Tyr	Gly	Leu	Asp	Ala	Trp
134				165						170					175	
136	Gly	Lys	Gly													

139 (2) INFORMATION FOR SEQ ID NO: 3:

141 (i) SEQUENCE CHARACTERISTICS:

142 (A) LENGTH: 543 base pairs

143 (B) TYPE: nucleic acid

144 (C) STRANDEDNESS: double

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145         (D) TOPOLOGY: linear
151     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
153 TCCCTTTCCC CAAGCGTCCA ANCCGTAGTA GTGGTCATAG TCACCCAGCA GGCTCTGTCT      60
155 TTCGCACAAG TAAAAGACAG CCGTGTCTCTC AGTTCTCAGC CTGTTCATTT TTAGATACAC      120
157 CGTGTTCTTG GAAGTGTCTC TGGAGATGGT GAATCGCCCC TTCACGGAGT CTGCGTAGTA      180
159 TTTAGTGCTT CCATCATATG ATATAACTGC CACCCACTCC AGCCCCTTGC CTAGAGCCTG      240
161 GCGGACCCAG TGCATAGCAA AGCTTCTGAA GGGGAATCCA GAGGCTGCAC AGGAGAGTCT      300
163 CAGGGACCTC CCAGGCTGGA CCAGCCTCC CCCAGACTCC ACCAGCTGCA CCTGACACTG      360
165 GATACCTCTT AAAAGAGCAA CGAGGAAAAC CCAGCTCAGC CCAAACCTCCA TGGTGAGTCC      420
167 TCTGTGTTCA GTGATGAAGC TTGAAATCAC TAGTGCGGCC GCCTGCAGGT CGACCATATG      480
169 GGAGAGCTCC CAACGCGTTG GATGCATAGC TTGAGTATTC TATAGTGTC CCTAAATAGC      540
171 TTG
173 (2) INFORMATION FOR SEQ ID NO: 4:
175     (i) SEQUENCE CHARACTERISTICS:
176         (A) LENGTH: 450 base pairs
177         (B) TYPE: nucleic acid
178         (C) STRANDEDNESS: double
179         (D) TOPOLOGY: linear
183     (ix) FEATURE:
184         (A) NAME/KEY: CDS
185         (B) LOCATION: 1..450
188     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
190 CTCGAGATGG ACATGGAGTT CCAGGCGCAG CTTCTCTTCC TCCTGCTACT CTGGCTCCCA      60
192 GATATCACCG GAGATATTGT GTTGACGCAG TCTCCAGGCA CCCTGTCTTT GTCTCCAGGG      120
194 GAAAGAGCCA CCCTCTCCTG CAGGGCCAGT CAGAGTGTTA GTAGCAGCTA CTTAGCCTGG      180
196 TACCAGCAGA AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATGGTGCATC CACCAGGGCC      240
198 ACTGGCATGC CAGACAGGTC CAGTGGCAGT GGGTCCGGGA CAGACTTCAC TCTCACCATC      300
200 AGTAGACTGG AGCCTGAAGA TTTTGCAGTG TATTACTGTC AGCAGTATGG TAGCTCACCT      360
202 CAGACACCTC AGATCACTTT CGGCGGAGGG ACCAAGGTGG AGATCAAACG AACTGTGGCT      420
204 GCACCATCTG TCTTCATCTT CCCGCCATCT
206 (2) INFORMATION FOR SEQ ID NO: 5:
208     (i) SEQUENCE CHARACTERISTICS:
209         (A) LENGTH: 150 amino acids
210         (B) TYPE: amino acid
211         (C) STRANDEDNESS: single
212         (D) TOPOLOGY: linear
218     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
220 Leu Glu Met Asp Met Glu Phe Gln Ala Gln Leu Leu Phe Leu Leu Leu
221 1 5 10 15
223 Leu Trp Leu Pro Asp Ile Thr Gly Asp Ile Val Leu Thr Gln Ser Pro
224 20 25 30
226 Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
227 35 40 45
229 Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
230 50 55 60
232 Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala
233 65 70 75 80
235 Thr Gly Met Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
236 85 90 95

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238   Thr Leu Thr  Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
239               100                      105                      110
241   Cys Gln Gln Tyr Gly Ser Ser  Pro Gln Thr  Pro Gln Ile Thr Phe Gly
242               115                      120                      125
244   Gly Gly Thr  Lys Val Glu Ile Lys Arg Thr  Val Ala Ala Pro Ser Val
245               130                      135                      140
247   Phe Ile Phe Pro Pro Ser
248       145                      150
250 (2) INFORMATION FOR SEQ ID NO: 6:
252   (i) SEQUENCE CHARACTERISTICS:
253       (A) LENGTH: 450 base pairs
254       (B) TYPE: nucleic acid
255       (C) STRANDEDNESS: double
256       (D) TOPOLOGY: linear
262   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
264 AGATGGCGGG AAGATGAAGA CAGATGGTGC AGCCACAGTT CGTTTGATCT CCACCTTGGT      60
266 CCCTCCGCCG AAAGTGATCT GAGGTGTCTG AGGTGAGCTA CCATACTGCT GACAGTAATA      120
268 CACTGCAAAA TCTTCAGGCT CCAGTCTACT GATGGTGAGA GTGAAGTCTG TCCCGGACCC      180
270 ACTGCCACTG AACCTGTCTG GCATGCCAGT GGCCCTGGTG GATGCACCAT AGATGAGGAG      240
272 CCTGGGAGCC TGGCCAGGTT TCTGCTGGTA CCAGGCTAAG TAGCTGCTAC TAACACTCTG      300
274 ACTGGCCCTG CAGGAGAGGG TGGCTCTTTC CCCTGGAGAC AAAGACAGGG TGCCTGGAGA      360
276 CTGCGTCAAC ACAATATCTC CGGTGATATC TGGGAGCCAG AGTAGCAGGA GGAAGAGAAG      420
278 CTGCGCCTGG AACTCCATGT CCATCTCGAG                                     450
280 (2) INFORMATION FOR SEQ ID NO: 7:
282   (i) SEQUENCE CHARACTERISTICS:
283       (A) LENGTH: 34 base pairs
284       (B) TYPE: nucleic acid
285       (C) STRANDEDNESS: single
286       (D) TOPOLOGY: linear
292   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
294 TATGAAGACA CCAGGCCGAT ATTGTGTTGA CGCA                                     34
296 (2) INFORMATION FOR SEQ ID NO: 8:
298   (i) SEQUENCE CHARACTERISTICS:
299       (A) LENGTH: 26 base pairs
300       (B) TYPE: nucleic acid
301       (C) STRANDEDNESS: single
302       (D) TOPOLOGY: linear
308   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
310 TATCCGGATG CAGCCACAGT TCGTTT                                     26
312 (2) INFORMATION FOR SEQ ID NO: 9:
314   (i) SEQUENCE CHARACTERISTICS:
315       (A) LENGTH: 26 base pairs
316       (B) TYPE: nucleic acid
317       (C) STRANDEDNESS: single
318       (D) TOPOLOGY: linear
324   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
326 TATTCGGACA GGTGCAGCTG GTGGAG                                     26
328 (2) INFORMATION FOR SEQ ID NO: 10:
330   (i) SEQUENCE CHARACTERISTICS:

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Input Set: N:\Crif3\RULE60\09194164.RAW.txt

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331      (A) LENGTH: 27 base pairs
332      (B) TYPE: nucleic acid
333      (C) STRANDEDNESS: single
334      (D) TOPOLOGY: linear
340      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
342 TATGGATCCT GAGGAGACGG TGACCGT                                27
344 (2) INFORMATION FOR SEQ ID NO: 11:
346      (i) SEQUENCE CHARACTERISTICS:
347          (A) LENGTH: 60 base pairs
348          (B) TYPE: nucleic acid
349          (C) STRANDEDNESS: single
350          (D) TOPOLOGY: linear
356      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
358 TATATATCCG GAGGTGGTGG ATCAGGTGGA GGTGGCTCCC AGGTGCAGCT GGTGGAGTCT    60
361 (2) INFORMATION FOR SEQ ID NO: 12:
363      (i) SEQUENCE CHARACTERISTICS:
364          (A) LENGTH: 46 base pairs
365          (B) TYPE: nucleic acid
366          (C) STRANDEDNESS: single
367          (D) TOPOLOGY: linear
373      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
375 ACCTCCGGAA CCGCCACCGC CAGAGACAGA TGGTGCAGCC ACATTC                    46
377 (2) INFORMATION FOR SEQ ID NO: 13:
379      (i) SEQUENCE CHARACTERISTICS:
380          (A) LENGTH: 918 base pairs
381          (B) TYPE: nucleic acid
382          (C) STRANDEDNESS: single
383          (D) TOPOLOGY: linear
387      (ix) FEATURE:
388          (A) NAME/KEY: CDS
389          (B) LOCATION: join(1..906, 913..918)
392      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
394 GAA TTC ATG AAA AAA ACC GCT ATC GCG ATC GCA GTT GCA CTG GCT GGT    48
395 Glu Phe Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly
396 1      5      10      15
398 TTC GCT ACC GTT GCG CAG GCC GAT ATT GTG TTG ACG CAG TCT CCA GGC    96
399 Phe Ala Thr Val Ala Gln Ala Asp Ile Val Leu Thr Gln Ser Pro Gly
400      20      25      30
402 ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC AGG GCC    144
403 Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
404      35      40      45
406 AGT CAG AGT GTT AGT AGC AGC TAC TTA GCC TGG TAC CAG CAG AAA CCT    192
407 Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
408      50      55      60
410 GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT GCA TCC ACC AGG GCC ACT    240
411 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
412 65      70      75      80
414 GGC ATG CCA GAC AGG TTC AGT GGC AGT GGG TCC GGG ACA GAC TTC ACT    288
415 Gly Met Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

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VERIFICATION SUMMARY

DATE: 09/15/2003

PATENT APPLICATION: US/09/194,164

TIME: 15:42:29

Input Set *: N:\Crf3\RULE60\09194164.RAW.txt

Output Set: N:\CRF4\09152003\I194164.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]